

Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Canceled).
2. (Currently amended) A method for identifying a nucleic acid binding protein's binding site on a region of a DNA or RNA comprising:
 - a) providing a nucleic acid ligand to ~~at~~the nucleic acid binding protein;
 - b) ~~contacting~~adding said nucleic acid ligand ~~with a mixture of~~to said nucleic acid binding protein and said DNA or RNA region; and
 - c) determining whether said added nucleic acid ligand ~~blocks~~inhibits said protein from binding to said RNA or DNA region, whereby the ~~presence~~sequence or structure of said inhibitory nucleic acid ligand assists in the identification of the binding site in the DNA or RNA ~~regulatory~~ region.
3. (Canceled).
4. (Currently amended) The method of claim 2 wherein said nucleic acid ligand is provided by the method comprising the steps of:
 - a) contacting a candidate mixture of nucleic acids each of which have a randomized sequence with the binding protein, whereby nucleic acids having an increased affinity to the protein relative to the candidate mixture may be partitioned from the remainder of the candidate mixture;
 - b) partitioning the increased affinity nucleic acids from the remainder of the candidate mixture; and
 - c) amplifying the increased affinity nucleic acids to yield a ligand-enriched mixture of nucleic acids, whereby a nucleic acid ligand of the protein may be identified.
5. (Previously presented) The method of claim 2 wherein the DNA or RNA region is

selected from the group consisting of a promoter, an origin of replication, a ribosomal binding site and a tRNA binding site.

6. (Previously presented) The method of claim 2 wherein the protein regulates transcription.

7. (Previously presented) The method of claim 2 wherein the protein regulates translation.

8. (Previously presented) The method of claim 2 wherein the protein is selected from the group consisting of transcriptional activators, transcriptional repressors, transcription complexes at promoter sites, replication accessory proteins, DNA polymerases, RNA polymerases and translational repressors.